

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/812,283

DATE: 07/30/2001

TIME: 12:09:15

Input Set : N:\Crif3\RULE60\09812283.txt

Output Set: N:\CRF3\07302001\I812283.raw

ENTERED

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3 <110> APPLICANT: Fischer, Robert L.
4 Ohad, Nir
5 Kiyosue, Tomohiro
6 Yadegari, Ramin
7 Margossian, Linda
8 Harada, John
9 Goldberg, Robert B.
10 The Regents of the University of California
12 <120> TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
13 Development in Plants
15 <130> FILE REFERENCE: 023070-086120US
17 <140> CURRENT APPLICATION NUMBER: 09/812,283
18 <141> CURRENT FILING DATE: 2001-03-19
20 <150> PRIOR APPLICATION NUMBER: 09/177,249
21 <151> PRIOR FILING DATE: 1998-10-22
23 <150> PRIOR APPLICATION NUMBER: US 09/071,838
24 <151> PRIOR FILING DATE: 1998-05-01
26 <160> NUMBER OF SEQ ID NOS: 324
28 <170> SOFTWARE: PatentIn Ver. 2.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2136
32 <212> TYPE: DNA
33 <213> ORGANISM: Arabidopsis sp.
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (43)..(2112)
38 <223> OTHER INFORMATION: fertilization-independent endosperm 1 (FIE1) cDNA
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43 1
45 aac cat gag gac gat ggt gag ggt ttg cca ccc gaa cta aat cag ata 102
46 Asn His Glu Asp Asp Gly Glu Gly Leu Pro Pro Glu Leu Asn Gln Ile
47 5 10 15 20
49 aaa gag caa atc gaa aag gag aga ttt ctg cat atc aag aga aaa ttc 150
50 Lys Glu Gln Ile Glu Lys Glu Arg Phe Leu His Ile Lys Arg Lys Phe
51 25 30 35
53 gag ctg aga tac att cca agt gtg gct act cat gct tca cac cat caa 198
54 Glu Leu Arg Tyr Ile Pro Ser Val Ala Thr His Ala Ser His His Gln
55 40 45 50
57 tcg ttt gac tta aac cag ccc gct gca gag gat gat aat gga gga gac 246
58 Ser Phe Asp Leu Asn Gln Pro Ala Ala Glu Asp Asp Asn Gly Gly Asp
59 55 60 65
61 aac aaa tca ctt ttg tcg aga atg caa aac cca ctt cgt cat ttc agt 294
62 Asn Lys Ser Leu Leu Ser Arg Met Gln Asn Pro Leu Arg His Phe Ser
63 70 75 80
65 gcc tca tct gat tat aat tct tac gaa gat caa ggt tat gtt ctt gat 342

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66 Ala Ser Ser Asp Tyr Asn Ser Tyr Glu Asp Gln Gly Tyr Val Leu Asp
67 85 90 95 100
69 gag gat caa gat tat gct ctt gaa gaa gat gta cca tta ttt ctt gat 390
70 Glu Asp Gln Asp Tyr Ala Leu Glu Glu Asp Val Pro Leu Phe Leu Asp
71 105 110 115
73 gaa gat gta cca tta tta cca agt gtc aag ctt cca att gtt gag aag 438
74 Glu Asp Val Pro Leu Leu Pro Ser Val Lys Leu Pro Ile Val Glu Lys
75 120 125 130
77 cta cca cga tcc att aca tgg gtc ttc acc aaa agt agc cag ctg atg 486
78 Leu Pro Arg Ser Ile Thr Trp Val Phe Thr Lys Ser Ser Gln Leu Met
79 135 140 145
81 gct gaa agt gat tct gtg att ggt aag aga caa atc tat tat ttg aat 534
82 Ala Glu Ser Asp Ser Val Ile Gly Lys Arg Gln Ile Tyr Tyr Leu Asn
83 150 155 160
85 ggt gag gca cta gaa ttg agc agt gaa gaa gat gag gaa gat gaa gaa 582
86 Gly Glu Ala Leu Glu Leu Ser Ser Glu Glu Asp Glu Glu Asp Glu Glu
87 165 170 175 180
89 gaa gat gag gaa gaa atc aag aaa gaa aaa tgc gaa ttt tct gaa gat 630
90 Glu Asp Glu Glu Glu Ile Lys Lys Glu Lys Cys Glu Phe Ser Glu Asp
91 185 190 195
93 gta gac cga ttt ata tgg acg gtt ggg cag gac tat ggt ttg gat gat 678
94 Val Asp Arg Phe Ile Trp Thr Val Gly Gln Asp Tyr Gly Leu Asp Asp
95 200 205 210
97 ctg gtc gtg cgg cgt gct ctc gcc aag tac ctc gaa gtg gat gtt tcg 726
98 Leu Val Val Arg Arg Ala Leu Ala Lys Tyr Leu Glu Val Asp Val Ser
99 215 220 225
101 gac ata ttg gaa aga tac aat gaa ctc aag ctt aag aat gat gga act 774
102 Asp Ile Leu Glu Arg Tyr Asn Glu Leu Lys Leu Lys Asn Asp Gly Thr
103 230 235 240
105 gct ggt gag gct tct gat ttg aca tcc aag aca ata act act gct ttc 822
106 Ala Gly Glu Ala Ser Asp Leu Thr Ser Lys Thr Ile Thr Thr Ala Phe
107 245 250 255 260
109 cag gat ttt gct gat aga cgt cat tgc cgt cgt tgc atg ata ttc gat 870
110 Gln Asp Phe Ala Asp Arg Arg His Cys Arg Arg Cys Met Ile Phe Asp
111 265 270 275
113 tgt cat atg cat gag aag tat gag ccc gag tct aga tcc agc gaa gac 918
114 Cys His Met His Glu Lys Tyr Glu Pro Glu Ser Arg Ser Ser Glu Asp
115 280 285 290
117 aaa tct agt ttg ttt gag gat gaa gat aga caa cca tgc agt gag cat 966
118 Lys Ser Ser Leu Phe Glu Asp Glu Asp Arg Gln Pro Cys Ser Glu His
119 295 300 305
121 tgt tac ctc aag gtg agg agt gtg aca gaa gct gat cat gtg atg gat 1014
122 Cys Tyr Leu Lys Val Arg Ser Val Thr Glu Ala Asp His Val Met Asp
123 310 315 320
125 aat gat aac tct ata tca aac aag att gtg gtc tca gat cca aac aac 1062
126 Asn Asp Asn Ser Ile Ser Asn Lys Ile Val Val Ser Asp Pro Asn Asn
127 325 330 335 340
129 act atg tgg acg cct gta gag aag gat ctt tac ttg aaa gga att gag 1110
130 Thr Met Trp Thr Pro Val Glu Lys Asp Leu Tyr Leu Lys Gly Ile Glu

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131		345		350		355	
133	ata ttt ggg aga aac agt tgt gat gtt gca tta aac ata ctt cgg ggg					1158	
134	Ile Phe Gly Arg Asn Ser Cys Asp Val Ala Leu Asn Ile Leu Arg Gly						
135		360		365		370	
137	ctt aag acg tgc cta gag att tac aat tac atg cgc gaa caa gat caa					1206	
138	Leu Lys Thr Cys Leu Glu Ile Tyr Asn Tyr Met Arg Glu Gln Asp Gln						
139		375		380		385	
141	tgt act atg tca tta gac ctt aac aaa act aca caa aga cac aat cag					1254	
142	Cys Thr Met Ser Leu Asp Leu Asn Lys Thr Thr Gln Arg His Asn Gln						
143		390		395		400	
145	gtt acc aaa aaa gta tct cga aaa agt agt agg tcg gtc cgc aaa aaa					1302	
146	Val Thr Lys Lys Val Ser Arg Lys Ser Ser Arg Ser Val Arg Lys Lys						
147		405		410		415	
149	tcg aga ctc cga aaa tat gct cgt tat ccg cct gct tta aag aaa aca					1350	
150	Ser Arg Leu Arg Lys Tyr Ala Arg Tyr Pro Pro Ala Leu Lys Lys Thr						
151		425		430		435	
153	act agt gga gaa gct aag ttt tat aag cac tac aca cca tgc act tgc					1398	
154	Thr Ser Gly Glu Ala Lys Phe Tyr Lys His Tyr Thr Pro Cys Thr Cys						
155		440		445		450	
157	aag tca aaa tgt gga cag caa tgc cct tgt tta act cac gaa aat tgc					1446	
158	Lys Ser Lys Cys Gly Gln Gln Cys Pro Cys Leu Thr His Glu Asn Cys						
159		455		460		465	
161	tgc gag aaa tat tgc ggg tgc tca aag gat tgc aac aat cgc ttt gga					1494	
162	Cys Glu Lys Tyr Cys Gly Cys Ser Lys Asp Cys Asn Asn Arg Phe Gly						
163		470		475		480	
165	gga tgt aat tgt gca att ggc caa tgc aca aat cga caa tgt cct tgt					1542	
166	Gly Cys Asn Cys Ala Ile Gly Gln Cys Thr Asn Arg Gln Cys Pro Cys						
167		485		490		495	
169	ttt gct gct aat cgt gaa tgc gat cca gat ctt tgt cgg agt tgt cct					1590	
170	Phe Ala Ala Asn Arg Glu Cys Asp Pro Asp Leu Cys Arg Ser Cys Pro						
171		505		510		515	
173	ctt agc tgt gga gat ggc act ctt ggt gag aca cca gtg caa atc caa					1638	
174	Leu Ser Cys Gly Asp Gly Thr Leu Gly Glu Thr Pro Val Gln Ile Gln						
175		520		525		530	
177	tgc aag aac atg caa ttc ctc ctt caa acc aat aaa aag att ctc att					1686	
178	Cys Lys Asn Met Gln Phe Leu Leu Gln Thr Asn Lys Lys Ile Leu Ile						
179		535		540		545	
181	gga aag tct gat gtt cat gga tgg ggt gca ttt aca tgg gac tct ctt					1734	
182	Gly Lys Ser Asp Val His Gly Trp Gly Ala Phe Thr Trp Asp Ser Leu						
183		550		555		560	
185	aaa aag aat gag tat ctc gga gaa tat act gga gaa ctg atc act cat					1782	
186	Lys Lys Asn Glu Tyr Leu Gly Glu Tyr Thr Gly Glu Leu Ile Thr His						
187		565		570		575	
189	gat gaa gct aat gag cgt ggg aga ata gaa gat cgg att ggt tct tcc					1830	
190	Asp Glu Ala Asn Glu Arg Gly Arg Ile Glu Asp Arg Ile Gly Ser Ser						
191		585		590		595	
193	tac ctc ttt acc ttg aat gat cag ctc gaa atc gat gct cgc cgt aaa					1878	
194	Tyr Leu Phe Thr Leu Asn Asp Gln Leu Glu Ile Asp Ala Arg Arg Lys						
195		600		605		610	

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197 gga aac gag ttc aaa ttt ctc aat cac tca gca aga cct aac tgc tac 1926
198 Gly Asn Glu Phe Lys Phe Leu Asn His Ser Ala Arg Pro Asn Cys Tyr
199      615      620      625
201 gcc aag ttg atg att gtg aga gga gat cag agg att ggt cta ttt gcg 1974
202 Ala Lys Leu Met Ile Val Arg Gly Asp Gln Arg Ile Gly Leu Phe Ala
203      630      635      640
205 gag aga gca atc gaa gaa ggt gag gag ctt ttc ttc gac tac tgc tat 2022
206 Glu Arg Ala Ile Glu Glu Gly Glu Glu Leu Phe Phe Asp Tyr Cys Tyr
207 645      650      655      660
209 gga cca gaa cat gcg gat tgg tcg cgt ggt cga gaa cct aga aag act 2070
210 Gly Pro Glu His Ala Asp Trp Ser Arg Gly Arg Glu Pro Arg Lys Thr
211      665      670      675
213 ggt gct tct aaa agg tct aag gaa gcc cgt cca gct cgt tagtttttga 2119
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215      680      685
217 tctgaggaga agcagca 2136
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222 <212> TYPE: PRT
223 <213> ORGANISM: Arabidopsis sp.
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230      20      25      30
232 Lys Arg Lys Phe Glu Leu Arg Tyr Ile Pro Ser Val Ala Thr His Ala
233      35      40      45
235 Ser His His Gln Ser Phe Asp Leu Asn Gln Pro Ala Ala Glu Asp Asp
236      50      55      60
238 Asn Gly Gly Asp Asn Lys Ser Leu Leu Ser Arg Met Gln Asn Pro Leu
239 65      70      75      80
241 Arg His Phe Ser Ala Ser Ser Asp Tyr Asn Ser Tyr Glu Asp Gln Gly
242      85      90      95
244 Tyr Val Leu Asp Glu Asp Gln Asp Tyr Ala Leu Glu Glu Asp Val Pro
245      100      105      110
247 Leu Phe Leu Asp Glu Asp Val Pro Leu Leu Pro Ser Val Lys Leu Pro
248      115      120      125
250 Ile Val Glu Lys Leu Pro Arg Ser Ile Thr Trp Val Phe Thr Lys Ser
251      130      135      140
253 Ser Gln Leu Met Ala Glu Ser Asp Ser Val Ile Gly Lys Arg Gln Ile
254 145      150      155      160
256 Tyr Tyr Leu Asn Gly Glu Ala Leu Glu Leu Ser Ser Glu Glu Asp Glu
257      165      170      175
259 Glu Asp Glu Glu Glu Asp Glu Glu Glu Ile Lys Lys Glu Lys Cys Glu
260      180      185      190
262 Phe Ser Glu Asp Val Asp Arg Phe Ile Trp Thr Val Gly Gln Asp Tyr
263      195      200      205
265 Gly Leu Asp Asp Leu Val Val Arg Arg Ala Leu Ala Lys Tyr Leu Glu
266      210      215      220

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268 Val Asp Val Ser Asp Ile Leu Glu Arg Tyr Asn Glu Leu Lys Leu Lys
269 225 230 235 240
271 Asn Asp Gly Thr Ala Gly Glu Ala Ser Asp Leu Thr Ser Lys Thr Ile
272 245 250 255
274 Thr Thr Ala Phe Gln Asp Phe Ala Asp Arg Arg His Cys Arg Arg Cys
275 260 265 270
277 Met Ile Phe Asp Cys His Met His Glu Lys Tyr Glu Pro Glu Ser Arg
278 275 280 285
280 Ser Ser Glu Asp Lys Ser Ser Leu Phe Glu Asp Glu Asp Arg Gln Pro
281 290 295 300
283 Cys Ser Glu His Cys Tyr Leu Lys Val Arg Ser Val Thr Glu Ala Asp
284 305 310 315 320
286 His Val Met Asp Asn Asp Asn Ser Ile Ser Asn Lys Ile Val Val Ser
287 325 330 335
289 Asp Pro Asn Asn Thr Met Trp Thr Pro Val Glu Lys Asp Leu Tyr Leu
290 340 345 350
292 Lys Gly Ile Glu Ile Phe Gly Arg Asn Ser Cys Asp Val Ala Leu Asn
293 355 360 365
295 Ile Leu Arg Gly Leu Lys Thr Cys Leu Glu Ile Tyr Asn Tyr Met Arg
296 370 375 380
298 Glu Gln Asp Gln Cys Thr Met Ser Leu Asp Leu Asn Lys Thr Thr Gln
299 385 390 395 400
301 Arg His Asn Gln Val Thr Lys Lys Val Ser Arg Lys Ser Ser Arg Ser
302 405 410 415
304 Val Arg Lys Lys Ser Arg Leu Arg Lys Tyr Ala Arg Tyr Pro Pro Ala
305 420 425 430
307 Leu Lys Lys Thr Thr Ser Gly Glu Ala Lys Phe Tyr Lys His Tyr Thr
308 435 440 445
310 Pro Cys Thr Cys Lys Ser Lys Cys Gly Gln Gln Cys Pro Cys Leu Thr
311 450 455 460
313 His Glu Asn Cys Cys Glu Lys Tyr Cys Gly Cys Ser Lys Asp Cys Asn
314 465 470 475 480
316 Asn Arg Phe Gly Gly Cys Asn Cys Ala Ile Gly Gln Cys Thr Asn Arg
317 485 490 495
319 Gln Cys Pro Cys Phe Ala Ala Asn Arg Glu Cys Asp Pro Asp Leu Cys
320 500 505 510
322 Arg Ser Cys Pro Leu Ser Cys Gly Asp Gly Thr Leu Gly Glu Thr Pro
323 515 520 525
325 Val Gln Ile Gln Cys Lys Asn Met Gln Phe Leu Leu Gln Thr Asn Lys
326 530 535 540
328 Lys Ile Leu Ile Gly Lys Ser Asp Val His Gly Trp Gly Ala Phe Thr
329 545 550 555 560
331 Trp Asp Ser Leu Lys Lys Asn Glu Tyr Leu Gly Glu Tyr Thr Gly Glu
332 565 570 575
334 Leu Ile Thr His Asp Glu Ala Asn Glu Arg Gly Arg Ile Glu Asp Arg
335 580 585 590
337 Ile Gly Ser Ser Tyr Leu Phe Thr Leu Asn Asp Gln Leu Glu Ile Asp
338 595 600 605
340 Ala Arg Arg Lys Gly Asn Glu Phe Lys Phe Leu Asn His Ser Ala Arg

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VERIFICATION SUMMARY

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Output Set: N:\CRF3\07302001\I812283.raw

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Input Set : N:\CrF3\RULE60\09812283.txt

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